

GenCore version 4.5  
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OW protein - protein search, using sw model

Run on: June 29, 2002, 08:24:26 ; Search time 64.65 Seconds

(without alignments)  
34.185 Million cell updates/sec

Title: US-09-787-097-12\_COPY\_1279\_1301  
Predict score: 116  
Sequence: 1 LVQPFVTFSCFLSLILVAAYVM 23

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

PIR.71:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	719	2 T00266	hypothetical prote
2	67	57.8	1291	2 T21694	hypothetical prote
3	56	48.3	1737	2 T00209	MEGF8 protein - hu
4	53	45.7	700	2 B84125	iron-sulphur-bind
5	52	44.8	150	2 S47459	probable membrane
6	52	44.8	434	2 AG0690	two component sens
7	51	44.0	273	2 A72378	conserved hypothet
8	50	43.1	430	2 B81263	probable ABC trans
9	50	43.1	433	2 C64917	terminator region
10	50	43.1	433	2 C90918	sensor histidine p
11	50	43.1	433	2 H85766	hypothetical prote
12	49.5	42.7	336	2 AH1212	TN16 ORF14 and to
13	49	42.2	262	2 S59078	conserved hypothet
14	49	42.2	387	2 G70337	Na+/H+-exchanging
15	48	41.4	180	2 B88134	hypothetical prote
16	48	41.4	180	2 AH3153	glycosyl transfera
17	48	41.4	320	2 A95187	hypothetical prote
18	48	41.4	338	1 S44207	sugar ABC transpo
19	48	41.4	344	2 H72418	hypothetical prote
20	48	41.4	366	2 S74387	hypothetical prote
21	48	41.4	379	2 AB2423	probable ABC trans
22	47.5	40.9	705	2 DB4680	trax protein - Esc
23	47	40.5	248	2 J01338	hypothetical prote
24	47	40.5	295	2 T16231	hypothetical prote
25	47	40.5	308	2 T24912	beta-carotene keto
26	47	40.5	320	2 S65078	hypothetical prote
27	47	40.5	347	2 A90318	hypothetical prote
28	47	40.5	352	2 A95098	hypothetical prote
29	47	40.5	360	2 A84944	hypothetical prote

30	47	40.5	361	2 E97965	hypothetical prote
31	47	40.5	364	2 D96973	spore germination
32	47	40.5	555	2 T17320	hypothetical prote
33	47	40.5	697	2 T18681	hypothetical prote
34	46.5	40.1	161	2 T20676	hypothetical prote
35	46.5	40.1	177	1 C64067	probable protein-d
36	46.5	40.1	267	2 D97565	transport protein
37	46.5	40.1	267	2 AB2786	SRG-independent pr
38	46.5	40.1	628	2 A99317	conserved hypothet
39	46	39.7	224	1 PMEF6	H+-transporting tw
40	46	39.7	363	2 B98054	glycosyl transfera
41	46	39.7	365	2 T33499	hypothetical prote
42	46	39.7	387	2 T49246	D4 dopamine recept
43	46	39.7	439	2 T50688	proline transport
44	46	39.7	1539	2 T30037	hypothetical prote
45	45	38.8	150	2 T12547	hypothetical prote

#### ALIGNMENTS

RESULT 1  
T00266  
hypothetical protein KIAA0534 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 21-Jul-2000  
C:Accession: T00266  
R:Nagase, T., Ishikawa, K., Miyajima, N., Tanaka, A., Kotani, H., Nomura, N., Ohara, A.  
DNA Res. 5, 31-39, 1998  
A>Title: Prediction of the coding sequences of unidentified human genes. IX. The comp  
A:Reference number: Z14086; MUID:98290545  
A:Accession: T00266  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-719 <NAC>  
A:Cross-references: EMBL:AB011106; NID:93043591; PIDN:BA025460.1; PID:93043592  
A:Experimental source: brain  
C:Genetics:  
A>Note: KIAA0534

Query Match  
Best Local Similarity 100.0%; Score 116; DB 2; Length 719;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LVQPFVTFSCFLSLILVAAYVM 23  
DB 570 LVQPFVTFSCFLSLILVAAYVM 592

RESULT 2  
T21694  
hypothetical protein F33C8.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T21694  
R:Percy, C.  
submitted to the EMBL Data Library, February 1996  
A:Reference number: Z19460  
A:Accession: T21694  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1291 <MIT>  
A:Cross-references: EMBL:Z69790; PIDN:CA093653.1; GSPDB:GN00028; CESP:F33C8.1  
C:Experimental source: clone F33C8  
C:Genetics:  
A:Gene: CESP:F33C8.1  
A:Map position: X  
A:Introns: 18/3; 61/3; 99/2; 128/3; 166/2; 204/2; 352/3; 439/1; 467/3; 549/1; 597/1;

Query Match  
Best Local Similarity 57.8%; Score 67; DB 2; Length 1291;  
54.5%; Pred. No. 0.14;